

**REMARKS**

Applicants have carefully studied the Office Action mailed on October 7, 2004, which issued in connection with this application. The present response is intended to be fully responsive to all points of rejection raised by the Examiner and is believed to place the claims in condition for allowance. Favorable reconsideration and allowance of the present claims are respectfully requested.

**Amendments to the Specification**

All amendments to the specification are of formal nature and are identical to the amendments introduced in the parent application Ser. No. 09/080,285 (U.S. Patent No. 6,040,181). No new subject matter has been added as a result of these amendments, no new search is required, and no new issues are raised.

**Pending Claims**

Claims 53 and 70-88 were pending and at issue in the application. Claims 53 and 76-81 have been allowed. Claims 70, 71 and 74 have been rejected under 35 U.S.C. §102(b) and/or 35 U.S.C. §102(e) as being anticipated by prior art. Claims 72, 73, 75, and 82-88 have been objected to as being dependent upon a rejected base claim.

Claim 71 has been canceled without prejudice or disclaimer. Applicants note for the record that the present amendment is made solely to expedite the prosecution and not as an admission of anticipation. Applicants reserve the right to pursue canceled subject matter in a continuing application.

Claim 70 has been amended by replacing the recitation “complementary to a portion of SEQ ID NO: 19” with the recitation “complementary to a portion of a human bcl-2 mRNA or a portion of







and 1563 (Fed. Cir. 1991); *University of Rochester v. G. D. Searle & Co., Inc.*, 358 F.3d 916, 921 (Fed. Cir. 2004); *Enzo Biochem, Inc. v. Gen-Probe Inc.*, 323 F.3d 956, 969 (Fed. Cir. 2002).

SEQ ID NO:19 as disclosed and claimed in the present application is the nucleic acid sequence of the human bcl-2 mRNA, while SEQ ID NO:20 and SEQ ID NO:22 are the two different coding (open reading frame) sequences resulting from alternative splicing of the primary human bcl-2 transcript. Applicants respectfully submit that these sequences were known at the time of filing of the '692 application and available to any person skilled in the art, *e.g.*, from the publication by Tsujimoto *et al.* (Proc. Natl. Acad. Sci. USA 1986, 83:5214-5218; attached as Exhibit A). Specifically, Figure 3A of the Tsujimoto reference discloses a nucleotide sequence of the 5.5-kb bcl-2 transcript, which is identical to SEQ ID NO: 19<sup>3</sup> (see Clustal W (1.82) sequence alignment attached as Exhibit B). Figure 3B of the Tsujimoto reference discloses a nucleotide sequence of the 3.5-kb bcl-2 transcript. The sequence corresponding to the open reading frame in this transcript is identical to SEQ ID NO: 22 (see Clustal W (1.82) sequence alignment attached as Exhibit C).

The Tsujimoto publication is referred to in various parts of the '692 application. For example, at page 17, lines 10-12, the '692 application discloses that "the human bcl-2 gene gives rise to several transcripts through alternative splice site selections, see Tsujimoto, et al., Proc. Natl. Acad. Sci. USA, 83:5214-5218, 1986". Furthermore, the '692 application discloses in the Examples at page 15, line 21 - page 16, line 2 that the human bcl-2 cDNA described in the Tsujimoto publication was used as a <sup>32</sup>P-labeled probe to identify bcl-2 transcripts by hybridization to cellular mRNA. In light of these references to the Tsujimoto publication, a person skilled in the art would have understood that SEQ ID NOS: 19, 20 and 22 were intended to be part of the '692 application as a source of sequence information for designing anticode oligomers complementary to strategic sites along a human bcl-2 mRNA or a human bcl-2 primary transcript.

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<sup>3</sup> SEQ ID NO: 19 is missing a poly A stretch at the very 3' end which is shown in Figure 3A of the Tsujimoto reference. This stretch is present in every mRNA and does not represent a unique portion of the sequence.



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